RAW SEQUENCE LISTING
ERROR REPORT

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form:

Application Serial Number: *10/678,588*

Source: *Ifwg*

Date Processed by STIC: *5/26/04*

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2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A
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FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT
MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

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Revised 05/17/04

IFWO

RAW SEQUENCE LISTING   DATE: 05/26/2004
PATENT APPLICATION: US/10/678,588   TIME: 15:38:44

Input Set : D:\52578C.ST25.txt
Output Set: N:\CRF4\05262004\J678588.raw


```
 3 <110> APPLICANT: Jingrui Wu
 5 <120> TITLE OF INVENTION: Water-Deficit-TolerantTransgenic Plants
 7 <130> FILE REFERENCE: 38-15(52578)C
C--> 9 <140> CURRENT APPLICATION NUMBER: US/10/678,588
C--> 9 <141> CURRENT FILING DATE: 2003-10-02
 9 <160> NUMBER OF SEQ ID NOS: 10
11 <170> SOFTWARE: PatentIn version 3.2
13 <210> SEQ ID NO: 1
14 <211> LENGTH: 2480
15 <212> TYPE: DNA
16 <213> ORGANISM: Artificial
18 <220> FEATURE:
19 <223> OTHER INFORMATION: transcriptional unit comprising promoter, coding sequence for
20        transcription factor of SEQ ID NO:2 and terminator elements
22 <400> SEQUENCE: 1
23 aggatattaa agtatgtatt catcattaat ataatcagtg tattccaata tgtactacga      60
25 tttccaatgt ctttattgtc gccgtatgta atcggcgtca caaaataatc cccggtgact     120
27 ttcttttaat ccaggatgaa ataaatatgtt attataattt ttgcgatttg gtccgttata    180
29 ggaattgaag tgtgcttgag ctcggtcgcc accactccca tttcataatt ttacatgtat     240
31 ttgaaaaata aaaatttatg gtattcaatt taaacacgta tacttgtaaa gaatgatatc     300
33 ttgaaagaaa tatagtttaa atatttattg ataaataac aagtcaggta ttatagtcca      360
35 agcaaaaaca taaatttatt gatgcaagtt taaattcaga aatatttcaa taactgatta     420
37 tatcagctgg tacattgccg tagatgaaag actgagtgcg atattatgtg taatacataa     480
39 attgatgata tagctagaac tagtggatcc cccgggccct gcaggctcga gctagtttga     540
41 gatatccccg ttatggtact ggggttgcat ataacccatt ccttggttgt atgctccctg     600
43 ttggcccatc ccttgtgcag ctgagctact tgctcccaca tgaccaaggg catccttttt     660
45 aattgagcca tcgctagatt ttgcagttaa cttgctatca ccctccatct ctctgtactt     720
47 ctgcaggtac accttgaggg gttcaatgta gtcttcaaac cccagcgtgg ccatggccca     780
49 cagcagatcg tcgccattga tggtcttccg cttctccctc tggcacttgt cactcgcttc     840
51 gctagtgatg aaggagatga actcggagac gcactcctgc acggtctcct tagcgtcctt     900
53 ggcgatcttc ccgttagccg ggatggtctt cccgttagcc gggatggcct tcttcatgat     960
55 gcgactgatg ttggcgatgg gcaggaacct gtcctgctcc ctgacgctgc caccgcctcc    1020
57 gcctcccctg gggctcccgc tctcgtggct cccgccgccg ccgccagggc tcgccggagc    1080
59 ttccgccatg gtctacctac aaaaaagctc cgcacgaggc tgcatttgtc acaaatcatg    1140
61 aaaagaaaaa ctaccgatga acaatgctga gggattcaaa ttctacccac aaaaagaaga    1200
63 aagaaagatc tagcacatct aagcctgacg aagcagcaga aatatataaa aatataaacc    1260
65 atagtgccct tttcccctct tcctgatctt gtttagcatg gcggaaattt taaacccccc    1320
67 atcatctccc ccaacaacgg cggatcgcag atctacatcc gagagcccca ttccccgcga    1380
69 gatccgggcc ggatccacgc cggcgagagc cccagccgcg agatcccgcc cctcccgcgc    1440
71 accgatctgg gcgcgcacga agccgcctct cgcccaccca aactaccaag gccaaagatc    1500
73 gagaccgaga cggaaaaaaa aaacggagaa agaaagagga gagggcgggg tggttaccg     1560
75 gcggcggcgg aggggggaggg gggaggagct cgtcgtccgg cagcgagggg ggaggaggtg   1620
77 gtggtggtgg tggtggtagg gttggggggga tgggaggaga ggggggggta tgtatatagt   1680
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 79 ggcgatgggg ggcgtttctt tggaagcgga gggagggccg gcctcgtcgc tggctcgcga   1740
 81 tcctcctcgc gtttccggcc cccacgaccc ggacccacct gctgtttttt cttttttttt   1800
 83 ttttcttttc ttttttttt tttggctgcg agacgtgcgg tgcgtgcgga caactcacgg   1860
 85 tgatagtggg ggggtgtgga gactattgtc cagttggctg gactggggtg ggttggggtg   1920
 87 ggttggggttg ggctgggctt gctatggatc gtggatagca ctttgggctt taggactta   1980
 89 ggggttgtttt ttgtaaatgt tttgagtcta agtttatctt ttatttttac tagaaaaaat   2040
 91 acccatgcgc tgcaacgggg gaaagctatt ttaatcttat tattgttcat tgtgagaatt   2100
 93 cgcctgaata tatatttttc tcaaaaatta tgtcaaatta gcatatgggt tttttttaaag   2160
 95 atatttctta tacaaatccc tctgtattta caaaagcaaa cgaacttaaa acccgactca   2220
 97 aatacagata tgcatttcca aaagcgaata aacttaaaaa ccaattcata caaaaatgac   2280
 99 gtatcaaagt accgacaaaa acatcctcaa ttttttataat agtagaaaag agtaaatttc   2340
101 actttgggcc accttttatt accgatattt tactttatac cacctttttaa ctgatgtttt   2400
103 cactttgac caggtaatct tacctttgtt ttattttgga ctatcccgac tctcttctca   2460
105 agcatatgaa tgacctcgag                                                 2480
108 <210> SEQ ID NO: 2
109 <211> LENGTH: 185
110 <212> TYPE: PRT
111 <213> ORGANISM: Zea mays
113 <400> SEQUENCE: 2
115 Met Ala Glu Ala Pro Ala Ser Pro Gly Gly Gly Gly Gly Ser His Glu
116 1               5                   10                  15
119 Ser Gly Ser Pro Arg Gly Gly Gly Gly Gly Gly Ser Val Arg Glu Gln
120             20                  25                  30
123 Asp Arg Phe Leu Pro Ile Ala Asn Ile Ser Arg Ile Met Lys Lys Ala
124         35                  40                  45
127 Ile Pro Ala Asn Gly Lys Thr Ile Pro Ala Asn Gly Lys Ile Ala Lys
128     50                  55                  60
131 Asp Ala Lys Glu Thr Val Gln Glu Cys Val Ser Glu Phe Ile Ser Phe
132 65                  70                  75                  80
135 Ile Thr Ser Glu Ala Ser Asp Lys Cys Gln Arg Glu Lys Arg Lys Thr
136             85                  90                  95
139 Ile Asn Gly Asp Asp Leu Leu Trp Ala Met Ala Thr Leu Gly Phe Glu
140             100                 105                 110
143 Asp Tyr Ile Glu Pro Leu Lys Val Tyr Leu Gln Lys Tyr Arg Glu Met
144         115                 120                 125
147 Glu Gly Asp Ser Lys Leu Thr Ala Lys Ser Ser Asp Gly Ser Ile Lys
148     130                 135                 140
151 Lys Asp Ala Leu Gly His Val Gly Ala Ser Ser Ser Ala Ala Gln Gly
152 145                 150                 155                 160
155 Met Gly Gln Gln Gly Ala Tyr Asn Gln Gly Met Gly Tyr Met Gln Pro
156             165                 170                 175
159 Gln Tyr His Asn Gly Asp Ile Ser Asn
160             180                 185
163 <210> SEQ ID NO: 3
164 <211> LENGTH: 178
165 <212> TYPE: PRT
166 <213> ORGANISM: Zea mays
168 <400> SEQUENCE: 3
170 Met Ala Glu Ala Pro Ala Ser Pro Gly Gly Gly Gly Gly Ser His Glu
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171 1               5               10              15
174 Ser Gly Ser Pro Arg Gly Gly Gly Gly Gly Ser Val Arg Glu Gln
175             20              25              30
178 Asp Arg Phe Leu Pro Ile Ala Asn Ile Ser Arg Ile Met Lys Lys Ala
179         35              40              45
182 Ile Pro Ala Asn Gly Lys Ile Ala Lys Asp Ala Lys Glu Thr Val Gln
183     50              55              60
186 Glu Cys Val Ser Glu Phe Ile Ser Phe Ile Thr Ser Glu Ala Ser Asp
187 65              70              75              80
190 Lys Cys Gln Arg Glu Lys Arg Lys Thr Ile Asn Gly Asp Asp Leu Leu
191             85              90              95
194 Trp Ala Met Ala Thr Leu Gly Phe Glu Asp Tyr Ile Glu Pro Leu Lys
195             100             105             110
198 Val Tyr Leu Gln Lys Tyr Arg Glu Met Glu Gly Asp Ser Lys Leu Thr
199         115             120             125
202 Ala Lys Ser Ser Asp Gly Ser Ile Lys Lys Asp Ala Leu Gly His Val
203     130             135             140
206 Gly Ala Ser Ser Ser Ala Ala Glu Gly Met Gly Gln Gln Gly Ala Tyr
207 145             150             155             160
210 Asn Gln Gly Met Gly Tyr Met Gln Pro Gln Tyr His Asn Gly Asp Ile
211             165             170             175
214 Ser Asn
218 <210> SEQ ID NO: 4
219 <211> LENGTH: 537
220 <212> TYPE: DNA
221 <213> ORGANISM: Zea mays
223 <400> SEQUENCE: 4
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226 aggggaggcg gaggcggtgg cagcgtcagg gagcaggaca ggttcctgcc catcgccaac     120
228 atcagtcgca tcatgaagaa ggccatcccg gctaacggga agatcgccaa ggacgctaag     180
230 gagaccgtgc aggagtgcgt ctccgagttc atctccttca tcactagcga agcgagtgac     240
232 aagtgccaga gggagaagcg gaagaccatc aatggcgacg atctgctgtg ggccatggcc     300
234 acgctggggt ttgaagacta cattgaaccc ctcaaggtgt acctacagaa gtacagagag     360
236 atggagggtg atagcaagtt aactgctaaa tctagcgatg gctcgattaa aaaggatgct     420
238 cttggtcatg tgggagcaag tagctcagct gcagaaggga tgggccaaca gggagcatac     480
240 aaccaaggaa tgggttatat gcaacctcag taccataacg gggatatctc aaactaa       537
243 <210> SEQ ID NO: 5
244 <211> LENGTH: 522
245 <212> TYPE: DNA
246 <213> ORGANISM: Glycine max
248 <400> SEQUENCE: 5
249 atgtcggatg cgccaccgag cccgactcat gagagtgggg gcgagcagag cccgcgcggt      60
251 tcgtcgtccg gcgcgaggga gcaggaccgg tacctcccga ttgccaacat cagccgcatt     120
253 atgaagaagg ctctgcctcc aacggcaag attgcaaagg atgccaaaga caccatgcag     180
255 gaatgcgttt ctgagttcat cagcttcatt accagcgagg cgagtgagaa atgccagaag     240
257 gagaagagaa agacaatcaa tggagacgat ttgctatggg ccatggccac tttaggattt     300
259 gaagactaca tagagccgct taaggtgtac ctggctaggt acagagaggc ggagggtgac     360
261 actaaaggat ctgctagaag tggtgatgga tctgctacac cagatcaagt tggccttgca     420
263 ggtcaaaatt ctcagcttgt tcatcagggt tcgctgaact atattggttt gcaggtgcaa     480
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265 ccacaacatc tggttatgcc ttcaatgcaa agccatgaat ag   522
268 <210> SEQ ID NO: 6
269 <211> LENGTH: 173
270 <212> TYPE: PRT
271 <213> ORGANISM: Glycine max
273 <400> SEQUENCE: 6
275 Met Ser Asp Ala Pro Pro Ser Pro Thr His Glu Ser Gly Gly Glu Gln
276 1   5   10   15
279 Ser Pro Arg Gly Ser Ser Ser Gly Ala Arg Glu Gln Asp Arg Tyr Leu
280   20   25   30
283 Pro Ile Ala Asn Ile Ser Arg Ile Met Lys Lys Ala Leu Pro Pro Asn
284   35   40   45
287 Gly Lys Ile Ala Lys Asp Ala Lys Asp Thr Met Gln Glu Cys Val Ser
288   50   55   60
291 Glu Phe Ile Ser Phe Ile Thr Ser Glu Ala Ser Glu Lys Cys Gln Lys
292 65   70   75   80
295 Glu Lys Arg Lys Thr Ile Asn Gly Asp Asp Leu Leu Trp Ala Met Ala
296   85   90   95
299 Thr Leu Gly Phe Glu Asp Tyr Ile Glu Pro Leu Lys Val Tyr Leu Ala
300   100   105   110
303 Arg Tyr Arg Glu Ala Glu Gly Asp Thr Lys Gly Ser Ala Arg Ser Gly
304   115   120   125
307 Asp Gly Ser Ala Thr Pro Asp Gln Val Gly Leu Ala Gly Gln Asn Ser
308   130   135   140
311 Gln Leu Val His Gln Gly Ser Leu Asn Tyr Ile Gly Leu Gln Val Gln
312 145   150   155   160
315 Pro Gln His Leu Val Met Pro Ser Met Gln Ser His Glu
316   165   170
319 <210> SEQ ID NO: 7
320 <211> LENGTH: 141
321 <212> TYPE: PRT
322 <213> ORGANISM: Arabidopsis thaliana
324 <400> SEQUENCE: 7
326 Met Ala Asp Thr Pro Ser Ser Pro Ala Gly Asp Gly Gly Glu Ser Gly
327 1   5   10   15
330 Gly Ser Val Arg Glu Gln Asp Arg Tyr Leu Pro Ile Ala Asn Ile Ser
331   20   25   30
334 Arg Ile Met Lys Lys Ala Leu Pro Pro Asn Gly Lys Ile Gly Lys Asp
335   35   40   45
338 Ala Lys Asp Thr Val Gln Glu Cys Val Ser Glu Phe Ile Ser Phe Ile
339   50   55   60
342 Thr Ser Glu Ala Ser Asp Lys Cys Gln Lys Glu Lys Arg Lys Thr Val
343 65   70   75   80
346 Asn Gly Asp Asp Leu Leu Trp Ala Met Ala Thr Leu Gly Phe Glu Asp
347   85   90   95
350 Tyr Leu Glu Pro Leu Lys Ile Tyr Leu Ala Arg Tyr Arg Glu Leu Glu
351   100   105   110
354 Gly Asp Asn Lys Gly Ser Gly Lys Ser Gly Asp Gly Ser Asn Arg Asp
355   115   120   125

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Output Set: N:\CRF4\05262004\J678588.raw

```
358 Ala Gly Gly Gly Val Ser Gly Glu Glu Met Pro Ser Trp
359       130               135               140
362 <210> SEQ ID NO: 8
363 <211> LENGTH: 100
364 <212> TYPE: PRT
365 <213> ORGANISM: Artificial
367 <220> FEATURE:
368 <223> OTHER INFORMATION: protein consensus sequence
371 <220> FEATURE:
372 <221> NAME/KEY: MISC_FEATURE
373 <223> OTHER INFORMATION: Xaa can be Ala or Pro
375 <220> FEATURE:
376 <221> NAME/KEY: MISC_FEATURE
377 <223> OTHER INFORMATION: Xaa can be Thr or none
379 <220> FEATURE:
380 <221> NAME/KEY: MISC_FEATURE
381 <223> OTHER INFORMATION: Xaa can be Ile or none
383 <220> FEATURE:
384 <221> NAME/KEY: MISC_FEATURE
385 <223> OTHER INFORMATION: Xaa can be Pro or none
387 <220> FEATURE:
388 <221> NAME/KEY: MISC_FEATURE
389 <223> OTHER INFORMATION: Xaa can be Ala or none
391 <220> FEATURE:
392 <221> NAME/KEY: MISC_FEATURE
393 <223> OTHER INFORMATION: Xaa can be Asn or none
395 <220> FEATURE:
396 <221> NAME/KEY: MISC_FEATURE
397 <223> OTHER INFORMATION: Xaa can be Gly or none
399 <220> FEATURE:
400 <221> NAME/KEY: MISC_FEATURE
401 <223> OTHER INFORMATION: Xaa can be Lys or none
403 <220> FEATURE:
404 <221> NAME/KEY: MISC_FEATURE
405 <223> OTHER INFORMATION: Xaa can be Glu or Asp
407 <220> FEATURE:
408 <221> NAME/KEY: MISC_FEATURE
409 <223> OTHER INFORMATION: Xaa can be Val or Met
411 <220> FEATURE:
412 <221> NAME/KEY: MISC_FEATURE
413 <223> OTHER INFORMATION: Xaa can be Asp or Glu
415 <220> FEATURE:
416 <221> NAME/KEY: MISC_FEATURE
417 <223> OTHER INFORMATION: Xaa can be Arg or Lys
419 <220> FEATURE:
420 <221> NAME/KEY: MISC_FEATURE
421 <223> OTHER INFORMATION: Xaa can be Gln or Ala
423 <220> FEATURE:
424 <221> NAME/KEY: MISC_FEATURE
```

pls insert Numeric identifier <221> and state the locations for each of the Xaa locations. pls see error explanation on pg. 7

RAW SEQUENCE LISTING ERROR SUMMARY   DATE: 05/26/2004
PATENT APPLICATION: US/10/678,588   TIME: 15:38:45

Input Set : D:\52578C.ST25.txt
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Please Note:
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the
Sequence Listing to ensure that a corresponding explanation is presented in the <220>
to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:8; Xaa Pos. 22,26,27,28,29,30,31,38,40,57,61,93,94,98
Seq#:9; Xaa Pos. 29
Seq#:10; Xaa Pos. 2,3,4,6

Invalid <213> Response:
Use of "Artificial" only as "<213> Organism" response is incomplete,
per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:1,8,9,10

VARIABLE LOCATION SUMMARY   DATE: 05/26/2004
PATENT APPLICATION: US/10/678,588   TIME: 15:38:45

Input Set : D:\52578C.ST25.txt
Output Set: N:\CRF4\05262004\J678588.raw

Error Explanation: ☐

Use of n's or Xaa's(NEW RULES):
Use of n's and/or Xaa's have been detected in the Sequence Listing.
Use of <220> to <223> is **MANDATORY** if n's or Xaa's are present.
in <220> to <223> section, please explain location of n or Xaa, and which
residue n or Xaa represents.

Seq#:8; Xaa Pos. 22,26,27,28,29,30,31,38,40,57,61,93,94,98
Seq#:9; Xaa Pos. 29
Seq#:10; Xaa Pos. 2,3,4,6

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<210> SEQ ID NO 9
<211> LENGTH: 55
<212> TYPE: PRT
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: consensus protein sequence
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<223> OTHER INFORMATION: Xaa can be Gln or Glu
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (29)..()
<223> OTHER INFORMATION: Xaa can be Gln or Glu
<400> SEQUENCE: 9
      Asp Ser Lys Leu Thr Ala Lys Ser Ser Asp Gly Ser Ile Lys Lys Asp
      1               5                   10                  15
      Ala Leu Gly His Val Gly Ala Ser Ser Ser Ala Ala Xaa Gly Met Gly
                  20                  25                  30
      Gln Gln Gly Ala Tyr Asn Gln Gly Met Gly Tyr Met Gln Pro Gln Tyr
                  35                  40                  45
      His Asn Gly Asp Ile Ser Asn
                  50                  55
```

(handwritten: delete — circling <221> NAME/KEY: MISC_FEATURE and <223> OTHER INFORMATION: Xaa can be Gln or Glu)

```
<210> SEQ ID NO 10
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: consensus protein sequence
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<223> OTHER INFORMATION: Xaa can be any naturally occuring amino acid
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (2)..(4)
<223> OTHER INFORMATION: Xaa can be any naturally occuring amino acid
<400> SEQUENCE: 10
      Met Xaa Xaa Xaa Pro Xaa Ser Pro
      1               5
```

(handwritten: delete — circling <221> NAME/KEY: MISC_FEATURE and <223> OTHER INFORMATION: Xaa can be any naturally occuring amino acid)

(handwritten: What about location 6?)

(handwritten: pls explain — circling Xaa at position 6)

(handwritten: pls see error explanation on pg. 7)

VERIFICATION SUMMARY   DATE: 05/26/2004
PATENT APPLICATION: **US/10/678,588**   TIME: 15:38:45

Input Set : **D:\52578C.ST25.txt**
Output Set: **N:\CRF4\05262004\J678588.raw**

```
L:9 M:270 C: Current Application Number differs, Replaced Current Application No
L:9 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:437 M:258 W: Mandatory Feature missing, <222> Tag not found for SEQ ID#:8
L:437 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:16
L:441 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:32
L:445 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:48
L:453 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:80
L:457 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:96
L:485 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9 after pos.:16
L:517 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10 after pos.:0
```